SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: Ullrich, Axel
                                  Aoki, Naohito
                                  Kim, Yeong Woong
                                  Wang, Hong Yang
                                  Chen, Zhengjun
                                  Naylor, Oliver
                                  Kharitonenkov, Alexei Igorevich

    (ii) TITLE OF INVENTION: NOVEL PTP20, PCP-2, BDP1, CLK,
                                  AND SIRP POLYPEPTIDES AND RELATED
                                  PRODUCTS AND METHODS

    (iii) NUMBER OF SEQUENCES: 38

    (iv) CORRESPONDENCE ADDRESS:

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        (C) CITY: Los Angeles
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        (E) COUNTRY: U.S.A.
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    (v) COMPUTER READABLE FORM:

        (A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                              storage
        (B) COMPUTER: IBM Compatible
        (C) OPERATING SYSTEM: IBM P.C. DOS 5.0
        (D) SOFTWARE: FastSEQ for Windows 2.0

    (vi) CURRENT APPLICATION DATA:

        (A) APPLICATION NUMBER: 08/877,150
        (B) FILING DATE: June 17, 1997
        (C) CLASSIFICATION:

    (vii) PRIOR APPLICATION DATA:

        (A) APPLICATION NUMBER: U.S. 60/019,629
        (B) FILING DATE: June 17, 1996

        (A) APPLICATION NUMBER: U.S. 60/023,485
        (B) FILING DATE: August 9, 1996

        (A) APPLICATION NUMBER: U.S. 60/030,860
        (B) FILING DATE: November 13, 1996

(A)	APPLICATION NUMBER:	U.S. 60/034,286
(B)	FILING DATE:	December 19, 1996
(A)	APPLICATION NUMBER:	U.S. 60/030,964
(B)	FILING DATE:	November 15, 1996

(viii) . ATTORNEY/AGENT INFORMATION:

(A)	NAME:	Warburg, Richard J.
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(C)	REFERENCE/DOCKET NUMBER:	225/298

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(2) INFORMATION FOR SEQ ID NO: 1:

   (i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	6 amino acids
(B)	TYPE:	amino acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY:	linear

   (ii) MOLECULE TYPE: peptide

   (ix) FEATURE:

      (D)   OTHER INFORMATION: "Xaa" in positions 3 and 5 stands
                                  for an unspecified amino acid.

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Phe Trp Xaa Met Xaa Trp
 1   5

(2) INFORMATION FOR SEQ ID NO: 2:

   (i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	7 amino acids
(B)	TYPE:	amino acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY:	linear

   (ii) MOLECULE TYPE: peptide

   (ix) FEATURE:

      (D)   OTHER INFORMATION: "Xaa" in position 6 stands for
                                  either Ser, Ile or Val.

SD-88184.1

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 2:

His Cys Ser Ala Gly Xaa Gly
 1   5

(2)   INFORMATION FOR SEQ ID NO: 3:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 6 amino acids
        (B)   TYPE: amino acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Phe Leu Glu Arg Leu Glu
 1   5

(2)   INFORMATION FOR SEQ ID NO: 4:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 6 amino acids
        (B)   TYPE: amino acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (ix) FEATURE:

        (D)   OTHER INFORMATION: "Xaa" in positions 3 and 5 stands
                                   for an unspecified amino acid.

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Arg Trp Xaa Met Xaa Trp
 1   5

(2)   INFORMATION FOR SEQ ID NO: 5:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 7 amino acids
        (B)   TYPE: amino acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide   .

(ix)   FEATURE:

    (D)   OTHER INFORMATION: "Xaa" in position 6 stands for
                                either Ser, Ile or Val.

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 5:

His Cys Ser Ala Gly Xaa Gly
1   5

(2)   INFORMATION FOR SEQ ID NO: 6:

  (i)   SEQUENCE CHARACTERISTICS:

    (A)   LENGTH: 27 base pairs
    (B)   TYPE: nucleic acid
    (C)   STRANDEDNESS: single
    (D)   TOPOLOGY: linear

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CTCTGTGTCC ACAGCAGTGC TGGCTGT   27

(2)   INFORMATION FOR SEQ ID NO: 7:

  (i)   SEQUENCE CHARACTERISTICS:

    (A)   LENGTH: 7 amino acids
    (B)   TYPE: amino acid
    (C)   STRANDEDNESS: single
    (D)   TOPOLOGY: linear

(ii)   MOLECULE TYPE: peptide

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 7:

His Arg Asp Leu Ala Ala Arg
1   5

(2)   INFORMATION FOR SEQ ID NO: 8:

  (i)   SEQUENCE CHARACTERISTICS:

    (A)   LENGTH: 6 amino acids
    (B)   TYPE: amino acid
    (C)   STRANDEDNESS: single
    (D)   TOPOLOGY: linear

(ii)   MOLECULE TYPE: peptide

(ix)   FEATURE:

    (D)   OTHER INFORMATION: "Xaa" in position 2 stands for
                                Val or Met. "Xaa" in position
                                5 stands for Tyr or Phe.

        (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Asp Xaa Trp Ser Xaa Gly
  1   5

(2)   INFORMATION FOR SEQ ID NO: 9:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 28 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CGGGATCCCT TCGCCTTGCA GCTTTGTC   28

(2)   INFORMATION FOR SEQ ID NO: 10:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 30 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CGGAATTCCT AGACTGATAC AGTCTGTAAG   30

(2)   INFORMATION FOR SEQ ID NO: 11:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 6 amino acids
        (B)   TYPE: amino acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (ii)   MOLECULE TYPE: peptide

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Asp Leu Lys Pro Glu Asn
  1   5

(2)   INFORMATION FOR SEQ ID NO: 12:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 6 amino acids
        (B)   TYPE: amino acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

109

113
167

```
(ii)   MOLECULE TYPE:        peptide

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO:  12:

Ala Met Met Glu Arg Ile
 1               5
```

```
(2)   INFORMATION FOR SEQ ID NO:  13:

   (i)   SEQUENCE CHARACTERISTICS:

         (A)   LENGTH:          30 base pairs
         (B)   TYPE:            nucleic acid
         (C)   STRANDEDNESS:    single
         (D)   TOPOLOGY:        linear

   (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:  13:

TATAGCGGCC GCTAGACTGA TACAGTCTGT                          30
```

```
(2)   INFORMATION FOR SEQ ID NO:  14:

   (i)   SEQUENCE CHARACTERISTICS:

         (A)   LENGTH:          32 base pairs
         (B)   TYPE:            nucleic acid
         (C)   STRANDEDNESS:    single
         (D)   TOPOLOGY:        linear

   (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:  14:

TCCCCCGGGA TGCCCCATCC CCGAAGGTAC CA                       32
```

```
(2)   INFORMATION FOR SEQ ID NO:  15:

   (i)   SEQUENCE CHARACTERISTICS:

         (A)   LENGTH:          39 base pairs
         (B)   TYPE:            nucleic acid
         (C)   STRANDEDNESS:    single
         (D)   TOPOLOGY:        linear

   (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:  15:

TATAGCGGCC GCTCACCGAC TGATATCCCG ACTGGAGTC                39
```

```
(2)   INFORMATION FOR SEQ ID NO:  16:

   (i)   SEQUENCE CHARACTERISTICS:

         (A)   LENGTH:          30 base pairs
         (B)   TYPE:            nucleic acid
         (C)   STRANDEDNESS:    single
         (D)   TOPOLOGY:        linear
```

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 16:

TCCCCCGGGG AGACGATGCA TCACTGTAAG   30

(2)   INFORMATION FOR SEQ ID NO: 17:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 39 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 17:

TATAGCGGCC GCGCTGGCCT GCACCTGTCA TCTGCTGGG   39

(2)   INFORMATION FOR SEQ ID NO: 18:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 30 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 18:

CGGAATTCAT GCGGCATTCC AAACGAACTC   30

(2)   INFORMATION FOR SEQ ID NO: 19:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 39 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TATAGCGGCC GCCCTGACTC CCACTCATTT CCTTTTTAA   39

(2)   INFORMATION FOR SEQ ID NO: 20:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 36 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 20:

CGGAATTCCG CCACCATGGC CCCTATACTA GGTTAT   36

(2)   INFORMATION FOR SEQ ID NO: 21:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 36 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GCCAAGCTTG CCACCATGGC CCCTATACTA GGTTAT   36

(2)   INFORMATION FOR SEQ ID NO: 22:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 21 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 22:

GTAGCAGTAA GAATAGTTAA A   21

(2)   INFORMATION FOR SEQ ID NO: 23:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 24 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 23:

GTTGCCCTGA GGATCATTAA GAAT   24

(2)   INFORMATION FOR SEQ ID NO: 24:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 24 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GTTGCCCTGA GGATCATCCG GAAT   24

(2)   INFORMATION FOR SEQ ID NO: 25:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 30 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 25:

TACAATTCTC ACTGCTACAT GTAAGCCATC   30

(2)   INFORMATION FOR SEQ ID NO: 26:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 13 amino acids
        (B)   TYPE: amino acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (ii)   MOLECULE TYPE: peptide

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Pro Ile Tyr Ser Phe Ile Gly Gly Glu His Phe Pro Arg
1   5   10

(2)   INFORMATION FOR SEQ ID NO: 27:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 9 amino acids
        (B)   TYPE: amino acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (ii)   MOLECULE TYPE: peptide

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Ile Val Glu Pro Asp Thr Glu Ile Lys
1   5

(2)   INFORMATION FOR SEQ ID NO: 28:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 6 amino acids
        (B)   TYPE: amino acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Tyr Gly Phe Ser Pro Arg
1   5

(2)   INFORMATION FOR SEQ ID NO: 29:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 12 amino acids
        (B)   TYPE: amino acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Ile Lys Glu Val Ala His Val Asn Leu Glu Val Arg
1   5   10

(2)   INFORMATION FOR SEQ ID NO: 30:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 8 amino acids
        (B)   TYPE: amino acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Val Ala Ala Gly Asp Ser Ala Thr
1   5

(2)   INFORMATION FOR SEQ ID NO: 31:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 2226 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

```
GAATTCCGGC ACGAGGCGGG TTGCAGTATG AGTCGCCAAT CGGACCTAGT GAGGAGCTTC   60
TTGGAGCAGC AGGAGGCCCG GGACCACCGG AAGGGGGCAA TCCTCGCCCG TGAGTTCAGC  120
GACATTAAGG CCCGCTCAGT GGCTTGGAAG ACTGAAGGTG TGTGCTCCAC TAAAGCCGGC  180
AGTCAGCAGG GAAACTCAAA GAAGAACCGC TACAAAGACG TGGTACCGTA TGATGAGACG  240
AGAGTCATCC TTTCCCTGCT CCAGGAGGAA GGACACGGAG ATTACATTAA TGCCAACTTC  300
ATCCGGGGCA CAGATGGAAG CCAGGCCTAC ATTGCGACGC AAGGACCCCT GCCTCACACT  360
CTGTTGGACT TCTGGCGCCT GGTTTGGGAG TTTGGAATCA AGGTGATCTT GATGGCCTGT  420
CAGGAGACAG AAAATGGACG GAGGAAGTGT GAACGCTACT GGGCCCAGGA GCGGGAGCCT  480
CTACAGGCCG GGCCTTTCTG CATCACCCTG ACAAAGGAGA CAGCACTGAC TTCGGACATC  540
ACTCTCAGGA CCCTCCAGGT TACATTCCAG AAGGAATCCC GTCCTGTGCA CCAGCTACAG  600
TACATGTCTT GGCCGGACCA CGGGGTTCCC AGCAGTTCCG ATCACATTCT CACCATGGTG  660
GAGGAGGCCC GTTGCCTCCA AGGACTTGGA CCTGGACCCC TCTGTGTCCA CTGCAGTGCT  720
GGCTGTGGAC AACAGGTGT CTTGTGTGCT GTTGATTACG TGAGGCAGTT GCTTCTGACT  780
CAGACAATCC CACCCAATTT CAGCCTCTTT GAAGTGGTCC TGGAGATGCG GAAACAGCGA  840
CCTGCAGCGG TGCAGACAGA GGAGCAGTAC AGGTTCCTGT ACCACACAGT GGCTCAGCTA  900
TTCTCCCGCA CTCTCCAGAA CAACAGTCCC CTCTACCAGA ACCTCAAGGA GAACCGCGCT  960
CCAATCTGCA AGGACTCCTC GTCCCTCAGG ACCTCCTCAG CCCTGCCTGC CACATCCCGC 1020
CCACTGGGTG GCGTTCTCAG GAGCATCTCG GTGCCTGGGC CACCGACCCT TCCCATGGCT 1080
GACACTTACG CTGTGGTGCA GAAGCGTGGC GCTTCCGGCA GCACAGGGCC GGGCACGCGG 1140
GCGCCCAACA GCACGGACAC CCCGATCTAC AGCCAGGTGG CTCCACGTAT CCAGCGGCCC 1200
GTGTCACACA CCGAAAACGC GCAGGGGACA ACGGCACTGG GCCGAGTTCC TGCGGATGAA 1260
AACCCTTCCG GGCCTGATGC CTATGAGGAA GTAACAGATG GAGCGCAGAC TGGTGGGCTA 1320
GGCTTCAACT TGCGCATTGG AAGACCTAAA GGGCCACGGG ATCCTCCAGC GGAGTGGACA 1380
CGGGTGTAAT GAGTGCTGTA CCAGTTCCAG CCTGTCACTC AGTGGTGGCT GGGCGACTGC 1440
AACCCCCATG CTGCTGTGTG CTGTCTTATG TATGAGTGGG ACTCATGGGC CTGAATCAAA 1500
ATAAAAGTTT CTCAGGGTAG AAAAAAACAA ATAGGGACTT TGGCCAGTGG TTATAGCAGT 1560
CAAAGCCAGG GGCTAGGAGG GGTAAGTGGG GGAGGTGGTG GATCTACTCT GAGAAAGTTT 1620
AGGAAAGCAC ATCAAGAGTG AGCATCGCCA CTCTTCTCCC CATACACCTA CTGGAAAGTG 1680
CACCCCAGAC AGAGTCCTAA CTTGACAGTG CACCTCAGAC AGGTCGCTAC CTGGATGGAC 1740
ATGCTGGCCC TACAGCTAGA GACATGTCTA ATTAGATCCT CATGTAAACT TGCAATGAGC 1800
TAGAAAGATC TCCGTCTGGT CAGGGAAATG GATCACCTAG TCAGGTAAAT AGTGTGCCAT 1860
CCAGÅAGACA GAACTGCAAG ATACCGTCTT TCTCAAAATG GAAGAAAATA GATCCTCAAG 1920
AATAAATGTA TGTACAATGC TCTACGCCCT GATCCTGCCC TGCCTCACTG CCATAATGTC 1980
ACAAACAAGT CAGGGTCTAT ATGACAGTTG TTCATCTAGT CAGTCCTGAC TGTGGCCTCT 2040
GCAGGCTCAG ATAGTGCCTT CTGCAGACTC TTGGAATGCC CGTCTTGAAC TTGATGAAAG 2100
CTTCTACCGG GAACTTGTAA ACATCATTAA AATTATTAAT GTAGAATTCA ATAAAGAGTG 2160
GGTCAAAAAC TCAAAAAAAA AAAAAAAAA AAAAAAAAC TCGAGAGTAC TTCTAGAGCG 2220
GGCGGG                                                          2226
```

(2) INFORMATION FOR SEQ ID NO: 32:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 453 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

```
Met Ser Arg Gln Ser Asp Leu Val Arg Ser Phe Leu Glu Gln Gln Glu
 1               5                  10                  15

Ala Arg Asp His Arg Lys Gly Ala Ile Leu Ala Arg Glu Phe Ser Asp
             20              25                  30
```

```
Ile Lys Ala Arg Ser Val Ala Trp Lys Thr Glu Gly Val Cys Ser Thr
    35                  40                  45

Lys Ala Gly Ser Gln Gln Gly Asn Ser Lys Lys Asn Arg Tyr Lys Asp
    50              55                  60

Val Val Pro Tyr Asp Glu Thr Arg Val Ile Leu Ser Leu Leu Gln Glu
65              70                  75                  80

Glu Gly His Gly Asp Tyr Ile Asn Ala Asn Phe Ile Arg Gly Thr Asp
            85                  90                  95

Gly Ser Gln Ala Tyr Ile Ala Thr Gln Gly Pro Leu Pro His Thr Leu
            100                 105                 110

Leu Asp Phe Trp Arg Leu Val Trp Glu Phe Gly Ile Lys Val Ile Leu
        115                 120                 125

Met Ala Cys Gln Glu Thr Glu Asn Gly Arg Arg Lys Cys Glu Arg Tyr
    130                 135                 140

Trp Ala Gln Glu Arg Glu Pro Leu Gln Ala Gly Pro Phe Cys Ile Thr
145                 150                 155                 160

Leu Thr Lys Glu Thr Ala Leu Thr Ser Asp Ile Thr Leu Arg Thr Leu
            165                 170                 175

Gln Val Thr Phe Gln Lys Glu Ser Arg Pro Val His Gln Leu Gln Tyr
            180                 185                 190

Met Ser Trp Pro Asp His Gly Val Pro Ser Ser Ser Asp His Ile Leu
        195                 200                 205

Thr Met Val Glu Glu Ala Arg Cys Leu Gln Gly Leu Gly Pro Gly Pro
    210                 215                 220

Leu Cys Val His Cys Ser Ala Gly Cys Gly Arg Thr Gly Val Leu Cys
225                 230                 235                 240

Ala Val Asp Tyr Val Arg Gln Leu Leu Leu Thr Gln Thr Ile Pro Pro
            245                 250                 255

Asn Phe Ser Leu Phe Glu Val Val Leu Glu Met Arg Lys Gln Arg Pro
            260                 265                 270

Ala Ala Val Gln Thr Glu Glu Gln Tyr Arg Phe Leu Tyr His Thr Val
    275                 280                 285

Ala Gln Leu Phe Ser Arg Thr Leu Gln Asn Asn Ser Pro Leu Tyr Gln
    290                 295                 300

Asn Leu Lys Glu Asn Arg Ala Pro Ile Cys Lys Asp Ser Ser Ser Leu
305                 310                 315                 320

Arg Thr Ser Ser Ala Leu Pro Ala Thr Ser Arg Pro Leu Gly Gly Val
            325                 330                 335

Leu Arg Ser Ile Ser Val Pro Gly Pro Pro Thr Leu Pro Met Ala Asp
            340                 345                 350
```

```
Thr Tyr Ala Val Val Gln Lys Arg Gly Ala Ser Gly Ser Thr Gly Pro
        355             360             365

Gly Thr Arg Ala Pro Asn Ser Thr Asp Thr Pro Ile Tyr Ser Gln Val
    370             375             380

Ala Pro Arg Ile Gln Arg Pro Val Ser His Thr Glu Asn Ala Gln Gly
385             390             395             400

Thr Thr Ala Leu Gly Arg Val Pro Ala Asp Glu Asn Pro Ser Gly Pro
            405             410             415

Asp Ala Tyr Glu Glu Val Thr Asp Gly Ala Gln Thr Gly Gly Leu Gly
        420             425             430

Phe Asn Leu Arg Ile Gly Arg Pro Lys Gly Pro Arg Asp Pro Pro Ala
        435             440             445

Glu Trp Thr Arg Val
    450
```

(2) INFORMATION FOR SEQ ID NO: 33:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 5581 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

```
AATTCCGGGC GCCAGTCCCG CTCCGCGCCG CGCCGCTCCG CTCCGGCTCG GGCTCCGGCT    60
CGCCTCGGGC TGGGCTCGGG CTCCGGGGGC GGCGTCCCCG CGCCGGGCCC CGGGACGCGC   120
CGACCTCCAA CCATGGCCCG TGCCCAGGCG CTCGTGCTGG CACTCACCTT CCAGCTCTGC   180
GCGCCGGAGA CCGAGACTCC GGCAGCTGGC TGCACCTTCG AGGAGGCAAG TGACCCAGCA   240
GTGCCCTGCG AGTACAGCCA GGCCCAGTAC GATGACTTCC AGTGGGAGCA AGTGCGAATC   300
CACCCTGGCA CCCGGGCACC TGCGGACCTG CCCCACGGCT CCTACTTGAT GGTCAACACT   360
TCCCAGCATG CCCCAGGCCA GCGAGCCCAT GTCATCTTCC AGAGCCTGAG CGAGAATGAT   420
ACCCACTGTG TGCAGTTCAG CTACTTCCTG TACAGCCGGG ACGGCACAGG CGGCACCCTG   480
CGCGTCTACG TGCGCGTTAA TGGGGGCCCC CTGGCGAGTG CTGTGTGGAA TATGACTGGA   540
TCCCACGGCC GTCAGTGGCA CCAGGCTGAG CTGGCTGTCA GCACTTTCTG GCCCAATGAA   600
TATCAGGTGC TGTTTGAGGC CCTCATCTCC CCAGACCGCA GGGGCTACAT GGGCCTAGAT   660
GACATCCTGC TTCTCAGCTA CCCCTGCGCA AAGGCCCCAC ACTTCTCCCG CCTGGGCGAC   720
GTGGAGGTCA ACGCGGGCCA GAACGCGTCG TTCCAGTGCA TGGCCGCGGG AGAGCCCATG   780
CGCCAACGCT TCCTCTTGCA ACGGCAGAGC GGGGCCCTGG TGCCGGCCGG GGCGTTCGGC   840
ACATCAGCCA CCGGCTTCCT GGCCACTTTC CCGCTGGCTG CCGTGAGCCG CGCCGAGCAG   900
GACCTGTACC GCTGTGTGTC CCAGGCCCCG CGCGGCGGCG TCTCTAACTT CCCGGGAGCTC   960
ATCGTCAAGG AGCCCCCAAC TCCCATCGCG CCCCCACAGC TGCTGCGTGC TGGCCCCACC  1020
TACCTCATCA TCCAGCTCAA CACCAACTCC ATCATTGGCG ACGGGCCGAT CGTGCGCAAG  1080
GAGATTGAGT ACCGCATGGC GCGCGGGCCC TGGGCTGAGG TGCACGCCGT CAGCCTGCAG  1140
ACCTACAAGC TGTGGCACCT CGACCCCGAC ACAGACTATG AGATCAGCGT GCTGCTCACG  1200
CGTCCCGGAG ACGGCGGCAC TGGCCGCTGG GCCACCCCTC ATCAGCCGCA CCAAATGCGC  1260
AGAGCCCATG AGGGCCCCAA AGGCCTGGCT TTTGCTGAGA TCCAGGCCCG TCAGCTGACC  1320
CTGCAGTGGG AACCACTGGG CTACAACGTG ACGCGTTGCC ACACCTATAC TGTGTCGCTG  1380
TGCTATCACT ACACCCTGGG CAGCAGCGCC AACCAGACCA TCCGAGAGTG TGTGAAGACA  1440
GAGCAAGGTG TCAGCCGCTA CACCATCAAG AACCTGCTGC CCTATCGGAA CGTTCACGTG  1500
AGGCTTGTCC TCACTAACCC TGAGGGGCGC AAAGAGGGCA AGGAGGTCAC TTTCCAGACG  1560
GATGAGGATG TGCCCAGTGG GATTGCAGCC GAGTCCCTGA CCTTCACTCC ACTGGAGGAC  1620
```

117

115

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ATGATCTTCC TCAAGTGGGA GGAGCCCCAG GAGCCCAATG GTCTCATCAC CCAGTATGAG   1680
ATCAGCTACC AGAGCATCGA GTCATCAGAC CCGGCAGTGA ACGTGCCAGG CCCACGACGT   1740
ACCATCTCCA AGCTCCGCAA TGAGACCTAC CATGTCTTCT CCAACCTGCA CCCAGGCACC   1800
ACCTACCTGT TCTCCGTGCG GGCCCGCACA GGCAAAGGCT TCGGCCAGGC GGCACTCACT   1860
GAGATAACCA CTAACATCTC TGCTCCCAGC TTTGATTATG CCGACATGCC GTCACCCCTG   1920
GGCGAGTCTG AGAACACCAT CACCGTGCTG CTGAGGCCGG CACAGGGCCG CGGTGCGCCC   1980
ATCAGTGTGT ACCAGGTGAT TGTGGAGGAG GAGCGGGCGC GAGGCTGCGG CGGGACGAGG   2040
TGGACAGGAC TGCTTCCCAG TGCCATTGAC CTTCGAGGCG GCGCTGGCCC CAGGCTGGTG   2100
CACTACTTCG GGGCCGAACT GGCGGCCAGC AGTCTACCTG AGGCCATGCC CTTTACCGTG   2160
GGTGACAACC AGACCTACCG AGGCTTCTGG AACCCACCAC TTGAGCCTAG GAAGGCCTAT   2220
CTCATCTACT TCCAGGCAGC AAGCCACCTG AAGGGGGAGA CCCGGCTGAA TTGCATCCGC   2280
ATTGCCAGGA AAGCTGCCTG CAAGGAAAGC AAGCGGCCCC TGGAGGTGTC CCAGAGATCG   2340
GAGGAGATGG GGCTTATCCT GGGCATCTGT GCAGGGGGGC TTGCTGTCCT CATCCTTCTC   2400
CTGGGTGCCA TCATTGTCAT CATCCGCAAA GGGAAGCCGG TGAACATGAC CAAGGCCACC   2460
GTCAACTACC GCCAGGAGAA GACACACATG ATCAGCGCCG TGGACCGCAG CTTCACAGAC   2520
CAGAGCACCC TGCAGGAGGA CGAGCGGCTG GGCCTGTCCT TCATGGACAC CCATGGCTAC   2580
AGCACCCGGG GAGACCAGCG CAGCGGTGGG GTCACTGAGG CCAGCAGCCT CCTGGGGGGC   2640
TCCCCGAGGC GTCCCTGTGG CCGGAAGGGC TCCCCATACA CACGGAGGCA GCTGCACCCT   2700
GCGGTGCGTG TCGCAGACCT TCTGCAGCAC ATCAACCAGA TGAAGACGGC CGAGGGTTAC   2760
GGCTTCAAGC AGGAGTATGA GAGCTTCTTT GAAGGCTGGG ACGCCACAAA GAAGAAAGAC   2820
AAGGTCAAGG GCAGCCGGCA GGAGCCAATG CCTGCCTATG ATCGGCACCG AGTGAAACTG   2880
CACCCGATGC TGGGAGACCC CAATGCCGAC TACATTAATG CCAACTACAT AGATGGTTAC   2940
CACAGGTCAA ACCACTTCAT AGCCACTCAA GGGCCGAAGC CTGAGATGGT CTATGACTTC   3000
TGGCGTATGG TGTGGCAGGA GCACTGTTCC AGCATCGTCA TGATCACCAA GCTGGTCGAG   3060
GTGGGCAGGG TGAAATGCTC ACGGTACTGG CCGGAGGACT CAGACACCTA CGGGGACATC   3120
AAGATTATGC TGGTGAAGAC AGAGACCCTG GCTGAGTATG TCGTGCGCAC TTTTGCCCTG   3180
GAGCGGAGAG GCTACTCTGC CCGGCACGAG GTCCGCCAGT CCCACTTCAC AGCGTGGCCA   3240
GAGCATGGCG TCCCCTACCA TGCCACGGGG CTGCTGGCTT TCATCCGGCG GGTGAAGGCC   3300
TCCACCCCAC CTGATGCCGG GCCCATTGTC ATCCACTGCA GCGCGGGCAC CGGCCGCACA   3360
CGTTGCTATA TCGTCCTGGA TGTGATGCTG GACATGGCAG AGTGTGAGGG CGTCGTGGAC   3420
ATTTACAACT GTGTGAAGAC TCTCTGCTCC CGGCGTGTCA ACATGATCCA GACTGAGGAG   3480
CAGTACATCT TCATTCATGA TGCAATCCTG GAGGCCTGCC TGTGTGGGGA GACCACCATC   3540
CCTGTCAGTG AGTTCAAGGC CACCTACAAG GAGATGATCC GCATTGATCC TCAGAGTAAT   3600
TCCTCCCAGC TGCGGGAAGA GTTCCAGACG CTGAACTCGG TCACCCCGCC GCTGGACGTG   3660
GAGGAGTGCA GCATCGCCCT GTTGCCCCGG AACCGCGACA AGAACCGCAG CATGGACGTC   3720
CTGCCGCCCG ACCGCTGCCT GCCCTTCCTC ATCTCCACTG ATGGGGACTC CAACAACTAC   3780
ATTAATGCAG CCCTGACTGA CAGCTACACA CGGAGGTCGG CCTTCATGGT GACCCTGCAC   3840
CCGCTGCAGA GCACCACGCC CGACTTCTGG CGGCTGGTCT ACGATTACGG GTGCACCTCC   3900
ATCGTCATGC TCAACCAGCT GAACCAGTCC AACTCCGCCT GGCCCTGCCT GCAGTACTGG   3960
CCAGAGCCAG GCCGGCAGCA ATATGGCCTC ATGGAGGTGG AGTTTATGTC GGGCACAGCT   4020
GATGAAGACT TAGTGGCTCG AGTCTTCCGG GTGCAGAACA TCTCTCGGTT GCAGGAGGGA   4080
GACCTGCTGG TGCGGCACTT CCAGTTCCTG CGCTGGTCTG CATACCGGGA CACACCTGAC   4140
TCCAAGAAGG CCTTCTTGCA CCTGCTGGCT GAGGTGGACA AGTGGCAGGC CGAGAGTGGG   4200
GATGGGCGCA CCATCGTGCA CTGCCTAAAC GGGGGAGGAC GCAGCGGCAC CTTCTGCGCC   4260
TGCGCCACGG TCCTGGAGAT GATCCGCTGC CACAACTTGG TGGACGTTTT CTTTGCTGCC   4320
CAAACCCTCC GGAACTACAA ACCCAACATG GTGGAGACCA TGGATCAGTA CCACTTTTGC   4380
TACGATGTGG CCCTGGAGTA CTTGGAGGGG CTGGAGTCAA GATAGCGGGG CCCTGGCCTG   4440
GGGCACCCAC TGCACACTCA GGGCCAGACC CACCATCCTG GACTGGCGAG GAAGATCAGT   4500
GCCTCCTGCT CTGCCCAAAC ACACTCCCAT GGGGCAAGCA CTGGAGTGGA TGCTGGGCTA   4560
TCTTGCTCCC CCTTCCACTG TGGGCAGGGC CTTTCGCTTG TCCCATGGGC GGGTGGTGGG   4620
CCAAGGAGGA GCTTAGCAAG TCTGCACCCC ACCCCACCT CCATAGGGTC CTGCAGGCCT   4680
GTGCTGAGAG GCCTGGTGCT GCCTGGCAGA GTGACAAAGG CTCAGGACGG CTGGCTCTGG   4740
GGGACTCAGG CCAAGGGGGT TGGCAGGATC CTGGGTTTTG GGAGGGATGA GTGAGGCCCT   4800
GCAGAGAGCA TCCCAGGCCA AGGTTCCCAC TCAGCCTGCC CCCTCTGCAT GTGGGTAGAG   4860
GATGTACTGG GACTTGGCAT TTAGGATTCC ATCTGGGGGA CCCCCTGAAG GTCCCCCCCA   4920
AGCAGGTCTC AATTCTGATA GCCAGTGGGG CACACTGACT GTCCTCCCCA GGGGAACTGC   4980
AGCGCCCTCC TCCCCACTGC CCCCTCCAGC CCCTGAGATA TTTTGCTCAC TATCCCTCCC   5040
CACTTGCTTC CCTGATATGT GCTCTGACTT CCCTGAACCA GGATCTGCCT ATTACTGCTG   5100
TCCCATGGGG GGCTCCTTCC CTGCCTGACC CACTGTTGCA GAATGAAGTC ACCTCGCCCC   5160
CCTCTTCCTT TAATCTTCAG GCCTCACTGG CCTGTCCTGC TCAGCTTGGG CCAGTGACAA   5220
TCTGCAAGGC TGAACAACAG CCCCTGGGGT TGAGGCCCCT GTGGCTCCTG GTCAGGCTGC   5280
CCGTTGTGGG GAGGGGCAGT GTTAGAGCAG GGCTGGTCAT ACCCTCTGGA GTTCAGAGCA   5340
```

116

118

```
AGAGGTAGGA CCAGTGCTTT TTTGTTTCTT TTGTTATTTT TGGTTGGGTG GGTGGGAAGG    5400
TCTCTTTAAA ATGGGGCAGG CCACACCCCC ATTCCGTGCC TCAATTTCCC CATCTGTAAA    5460
CTGTAGATAT GACTACTGAC CTACCTCGCA GGGGGCTGTG GGGAGGCATA AGCTGATGTT    5520
TGTAAAGCGC TTTGTAAATA AACGTGCTCT CTGAATGCCA AAAAAAAAAA AACAAAAAAA    5580
A                                                                   5581
```

(2) INFORMATION FOR SEQ ID NO: 34:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 1430 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

```
Met Ala Arg Ala Gln Ala Leu Val Leu Ala Leu Thr Phe Gln Leu Cys
 1           5              10              15

Ala Pro Glu Thr Glu Thr Pro Ala Ala Gly Cys Thr Phe Glu Glu Ala
            20              25              30

Ser Asp Pro Ala Val Pro Cys Glu Tyr Ser Gln Ala Gln Tyr Asp Asp
            35              40              45

Phe Gln Trp Glu Gln Val Arg Ile His Pro Gly Thr Arg Ala Pro Ala
    50              55              60

Asp Leu Pro His Gly Ser Tyr Leu Met Val Asn Thr Ser Gln His Ala
65              70              75              80

Pro Gly Gln Arg Ala His Val Ile Phe Gln Ser Leu Ser Glu Asn Asp
            85              90              95

Thr His Cys Val Gln Phe Ser Tyr Phe Leu Tyr Ser Arg Asp Gly Thr
            100             105             110

Gly Gly Thr Leu Arg Val Tyr Val Arg Val Asn Gly Gly Pro Leu Ala
            115             120             125

Ser Ala Val Trp Asn Met Thr Gly Ser His Gly Arg Gln Trp His Gln
    130             135             140

Ala Glu Leu Ala Val Ser Thr Phe Trp Pro Asn Glu Tyr Gln Val Leu
145             150             155             160

Phe Glu Ala Leu Ile Ser Pro Asp Arg Arg Gly Tyr Met Gly Leu Asp
                165             170             175

Asp Ile Leu Leu Leu Ser Tyr Pro Cys Ala Lys Ala Pro His Phe Ser
            180             185             190

Arg Leu Gly Asp Val Glu Val Asn Ala Gly Gln Asn Ala Ser Phe Gln
            195             200             205

Cys Met Ala Ala Gly Glu Pro Met Arg Gln Arg Phe Leu Leu Gln Arg
    210             215             220
```

```
Gln Ser Gly Ala Leu Val Pro Ala Gly Ala Phe Gly Thr Ser Ala Thr
225             230             235             240

Gly Phe Leu Ala Thr Phe Pro Leu Ala Ala Val Ser Arg Ala Glu Gln
            245             250             255

Asp Leu Tyr Arg Cys Val Ser Gln Ala Pro Arg Gly Gly Val Ser Asn
            260             265             270

Phe Pro Glu Leu Ile Val Lys Glu Pro Pro Thr Pro Ile Ala Pro Pro
        275             280             285

Gln Leu Leu Arg Ala Gly Pro Thr Tyr Leu Ile Ile Gln Leu Asn Thr
    290             295             300

Asn Ser Ile Ile Gly Asp Gly Pro Ile Val Arg Lys Glu Ile Glu Tyr
305             310             315             320

Arg Met Ala Arg Gly Pro Trp Ala Glu Val His Ala Val Ser Leu Gln
            325             330             335

Thr Tyr Lys Leu Trp His Leu Asp Pro Asp Thr Asp Tyr Glu Ile Ser
            340             345             350

Val Leu Leu Thr Arg Pro Gly Asp Gly Gly Thr Gly Arg Trp Ala Thr
            355             360             365

Pro His Gln Pro His Gln Met Arg Arg Ala His Glu Gly Pro Lys Gly
    370             375             380

Leu Ala Phe Ala Glu Ile Gln Ala Arg Gln Leu Thr Leu Gln Trp Glu
385             390             395             400

Pro Leu Gly Tyr Asn Val Thr Arg Cys His Thr Tyr Thr Val Ser Leu
            405             410             415

Cys Tyr His Tyr Thr Leu Gly Ser Ser His Asn Gln Thr Ile Arg Glu
            420             425             430

Cys Val Lys Thr Glu Gln Gly Val Ser Arg Tyr Thr Ile Lys Asn Leu
            435             440             445

Leu Pro Tyr Arg Asn Val His Val Arg Leu Val Leu Thr Asn Pro Glu
    450             455             460

Gly Arg Lys Glu Gly Lys Glu Val Thr Phe Gln Thr Asp Glu Asp Val
465             470             475             480

Pro Ser Gly Ile Ala Ala Glu Ser Leu Thr Phe Thr Pro Leu Glu Asp
            485             490             495

Met Ile Phe Leu Lys Trp Glu Glu Pro Gln Glu Pro Asn Gly Leu Ile
            500             505             510

Thr Gln Tyr Glu Ile Ser Tyr Gln Ser Ile Glu Ser Ser Asp Pro Ala
    515             520             525

Val Asn Val Pro Gly Pro Arg Arg Thr Ile Ser Lys Leu Arg Asn Glu
    530             535             540
```

```
Thr Tyr His Val Phe Ser Asn Leu His Pro Gly Thr Thr Tyr Leu Phe
545                 550             555                 560

Ser Val Arg Ala Arg Thr Gly Lys Gly Phe Gly Gln Ala Ala Leu Thr
                565             570                 575

Glu Ile Thr Thr Asn Ile Ser Ala Pro Ser Phe Asp Tyr Ala Asp Met
            580             585                 590

Pro Ser Pro Leu Gly Glu Ser Glu Asn Thr Ile Thr Val Leu Leu Arg
        595             600                 605

Pro Ala Gln Gly Arg Gly Ala Pro Ile Ser Val Tyr Gln Val Ile Val
    610             615                 620

Glu Glu Glu Arg Ala Arg Gly Cys Gly Gly Thr Arg Trp Thr Gly Leu
625             630                 635                 640

Leu Pro Ser Ala Ile Asp Leu Arg Gly Gly Ala Gly Pro Arg Leu Val
            645             650                 655

His Tyr Phe Gly Ala Glu Leu Ala Ala Ser Ser Leu Pro Glu Ala Met
        660             665                 670

Pro Phe Thr Val Gly Asp Asn Gln Thr Tyr Arg Gly Phe Trp Asn Pro
        675             680                 685

Pro Leu Glu Pro Arg Lys Ala Tyr Leu Ile Tyr Phe Gln Ala Ala Ser
    690             695                 700

His Leu Lys Gly Glu Thr Arg Leu Asn Cys Ile Arg Ile Ala Arg Lys
705             710             715                 720

Ala Ala Cys Lys Glu Ser Lys Arg Pro Leu Glu Val Ser Gln Arg Ser
            725             730                 735

Glu Glu Met Gly Leu Ile Leu Gly Ile Cys Ala Gly Gly Leu Ala Val
        740             745                 750

Leu Ile Leu Leu Leu Gly Ala Ile Ile Val Ile Ile Arg Lys Gly Lys
    755             760                 765

Pro Val Asn Met Thr Lys Ala Thr Val Asn Tyr Arg Gln Glu Lys Thr
    770             775                 780

His Met Ile Ser Ala Val Asp Arg Ser Phe Thr Asp Gln Ser Thr Leu
785             790             795                 800

Gln Glu Asp Glu Arg Leu Gly Leu Ser Phe Met Asp Thr His Gly Tyr
            805             810                 815

Ser Thr Arg Gly Asp Gln Arg Ser Gly Gly Val Thr Glu Ala Ser Ser
        820             825                 830

Leu Leu Gly Gly Ser Pro Arg Arg Pro Cys Gly Arg Lys Gly Ser Pro
        835             840                 845

Tyr His Thr Gly Gln Leu His Pro Ala Val Arg Val Ala Asp Leu Leu
    850             855                 860

Gln His Ile Asn Gln Met Lys Thr Ala Glu Gly Tyr Gly Phe Lys Gln
865             870             875                 880
```

Glu Tyr Glu Ser Phe Phe Glu Gly Trp Asp Ala Thr Lys Lys Lys Asp
            885   890   895

Lys Val Lys Gly Ser Arg Gln Glu Pro Met Pro Ala Tyr Asp Arg His
            900   905   910

Arg Val Lys Leu His Pro Met Leu Gly Asp Pro Asn Ala Asp Tyr Ile
        915   920   925

Asn Ala Asn Tyr Ile Asp Gly Tyr His Arg Ser Asn His Phe Ile Ala
    930   935   940

Thr Gln Gly Pro Lys Pro Glu Met Val Tyr Asp Phe Trp Arg Met Val
945   950   955   960

Trp Gln Glu His Cys Ser Ser Ile Val Met Ile Thr Lys Leu Val Glu
            965   970   975

Val Gly Arg Val Lys Cys Ser Arg Tyr Trp Pro Glu Asp Ser Asp Thr
            980   985   990

Tyr Gly Asp Ile Lys Ile Met Leu Val Lys Thr Glu Thr Leu Ala Glu
            995   1000   1005

Tyr Val Val Arg Thr Phe Ala Leu Glu Arg Arg Gly Tyr Ser Ala Arg
    1010   1015   1020

His Glu Val Arg Gln Ser His Phe Thr Ala Trp Pro Glu His Gly Val
1025   1030   1035   1040

Pro Tyr His Ala Thr Gly Leu Leu Ala Phe Ile Arg Arg Val Lys Ala
            1045   1050   1055

Ser Thr Pro Pro Asp Ala Gly Pro Ile Val Ile His Cys Ser Ala Gly
            1060   1065   1070

Thr Gly Arg Thr Arg Cys Tyr Ile Val Leu Asp Val Met Leu Asp Met
        1075   1080   1085

Ala Glu Cys Glu Gly Val Val Asp Ile Tyr Asn Cys Val Lys Thr Leu
    1090   1095   1100

Cys Ser Arg Arg Val Asn Met Ile Gln Thr Glu Glu Gln Tyr Ile Phe
1105   1110   1115   1120

Ile His Asp Ala Ile Leu Glu Ala Cys Leu Cys Gly Glu Thr Thr Ile
            1125   1130   1135

Pro Val Ser Glu Phe Lys Ala Thr Tyr Lys Glu Met Ile Arg Ile Asp
            1140   1145   1150

Pro Gln Ser Asn Ser Ser Gln Leu Arg Glu Glu Phe Gln Thr Leu Asn
            1155   1160   1165

Ser Val Thr Pro Pro Leu Asp Val Glu Glu Cys Ser Ile Ala Leu Leu
    1170   1175   1180

Pro Arg Asn Arg Asp Lys Asn Arg Ser Met Asp Val Leu Pro Pro Asp
    1185   1190   1195   1200

```
Arg Cys Leu Pro Phe Leu Ile Ser Thr Asp Gly Asp Ser Asn Asn Tyr
          1205              1210          1215

Ile Asn Ala Ala Leu Thr Asp Ser Tyr Thr Arg Arg Ser Ala Phe Met
          1220              1225          1230

Val Thr Leu His Pro Leu Gln Ser Thr Thr Pro Asp Phe Trp Arg Leu
          1235              1240          1245

Val Tyr Asp Tyr Gly Cys Thr Ser Ile Val Met Leu Asn Gln Leu Asn
          1250              1255          1260

Gln Ser Asn Ser Ala Trp Pro Cys Leu Gln Tyr Trp Pro Glu Pro Gly
     1265              1270          1275              1280

Arg Gln Gln Tyr Gly Leu Met Glu Val Glu Phe Met Ser Gly Thr Ala
               1285              1290              1295

Asp Glu Asp Leu Val Ala Arg Val Phe Arg Val Gln Asn Ile Ser Arg
          1300              1305              1310

Leu Gln Glu Gly Asp Leu Leu Val Arg His Phe Gln Phe Leu Arg Trp
          1315              1320              1325

Ser Ala Tyr Arg Asp Thr Pro Asp Ser Lys Lys Ala Phe Leu His Leu
     1330              1335              1340

Leu Ala Glu Val Asp Lys Trp Gln Ala Glu Ser Gly Asp Gly Arg Thr
     1345              1350              1355              1360

Ile Val His Cys Leu Asn Gly Gly Gly Arg Ser Gly Thr Phe Cys Ala
               1365              1370              1375

Cys Ala Thr Val Leu Glu Met Ile Arg Cys His Asn Leu Val Asp Val
               1380              1385              1390

Phe Phe Ala Ala Gln Thr Leu Arg Asn Tyr Lys Pro Asn Met Val Glu
          1395              1400              1405

Thr Met Asp Gln Tyr His Phe Cys Tyr Asp Val Ala Leu Glu Tyr Leu
     1410              1415              1420

Glu Gly Leu Glu Ser Arg
1425              1430
```

(2)   INFORMATION FOR SEQ ID NO: 35:

   (i)   SEQUENCE CHARACTERISTICS:

         (A)   LENGTH: 2810 base pairs
         (B)   TYPE: nucleic acid
         (C)   STRANDEDNESS: single
         (D)   TOPOLOGY: linear

   (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 35:

```
GAATTCGGCA CGAGCGGGCT GGACCTTGCT CGCCCGCGGC GCCATGAGCC GCAGCCTGGA      60
CTCGGCGCGG AGCTTCCTGG AGCGGCTGGA AGCGCGGGGC GGCCGGGAGG GGGCAGTCCT     120
CGCCGGCGAG TTCAGCGACA TCCAGGCCTG CTCGGCCGCC TGGAAGGCTG ACGGCGTGTG     180
```

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CTCCACCGTG GCCGGCAGTC GGCCAGAGAA CGTGAGGAAG AACCGCTACA AAGACGTGCT    240
GCCTTATGAT CAGACGCGAG TAATCCTCTC CCTGCTCCAG GAAGAGGGAC ACAGCGACTA    300
CATTAATGGC AACTTCATCC GGGGCGTGGA TGGAAGCCTG GCCTACATTG CCACGCAAGG    360
ACCCTTGCCT CACACCCTGC TAGACTTCTG GAGACTGGTC TGGGAGTTTG GGGTCAAGGT    420
GATCCTGATG GCCTGTCGAG AGATAGAGAA TGGGCGGAAA AGGTGTGAGC GGTACTGGGC    480
CCAGGAGCAG GAGCCACTGC AGACTGGGCT TTTCTGCATC ACTCTGATAA AGGAGAAGTG    540
GCTGAATGAG GACATCATGC TCAGGACCCT CAAGGTCACA TTCCAGAAGG AGTCCCGTTC    600
TGTGTACCAG CTACAGTATA TGTCCTGGCC AGACCGTGGG GTCCCCAGCA GTCCTGACCA    660
CATGCTCGCC ATGGTGGAGG AAGCCCGTCG CCTCCAGGGA TCTGGCCCTG AACCCTCTG     720
TGTCCACTGC AGTGCGGGTT GTGGGCGAAC AGGCGTCCTG TGCACCGTGG ATTATGTGAG    780
GCAGCTGCTC CTGACCCAGA TGATCCCACC TGACTTCAGT CTCTTTGATG TGGTCCTTAA    840
GATGAGGAAG CAGCGGCCTG CGGCCGTGCA GACAGAGGAG CAGTACAGGT TCCTGTACCA    900
CACGGTGGCT CAGATGTTCT GCTCCACACT CCAGAATGCC AGCCCCCACT ACCAGAACAT    960
CAAAGAGAAT TGTGCCCCAC TCTACGACGA TGCCCTCTTC CTCCGGACTC CCCAGGCACT   1020
TCTCGCCATA CCCCGCCCAC CAGGAGGGGT CCTCAGGAGC ATCTCTGTGC CCGGGTCCCC   1080
GGGCCACGCC ATGGCTGACA CCTACGCGGA GGAGCAGAAG CGCGGGGCTC CAGCGGGCGC   1140
CGGGAGTGGG ACGCAGACGG GGACGGGGAC GGGGGCGCGC AGCGCGGAGG AGGCGCCGCT   1200
CTACAGCAAG GTGACGCCGC GCGCCCAGCG ACCCGGGGCG CACGCGGAGG ACGCGAGGGG   1260
GACGCTGCCT GGCCGCGTTC CTGCTGACCA AAGTCCTGCC GGATCTGGCG CCTACGAGGA   1320
CGTGGCGGGT GGAGCTCAGA CCGGTGGGCT AGGTTTCAAC CTGCGCATTG GGAGGCCGAA   1380
GGGTCCCCGG GACCCGCCTG CTGAGTGGAC CCGGGTGTAA GTCTAACGCC AGTTCCTGCC   1440
TGTTGCCTCT TGTGAGCTCG GACTGCTGAT GCCCCGGTGC TGCTGAGCGC CGTGCCGAGA   1500
ATGGAAACAG TGGGCCTGGA TCAAAGTTAA AGTTTCTCAG GGTGGGAAAT GTGGGGGCTT   1560
TGCCCAATGA CTGTAGCATT CAAGGCTTGA GGCTGGAGGA GGTAGCTAGG GTATAGTGGC   1620
TGGTGAGGCT GCACAGAGCA GATTCAAGAA AGAAGATCAG GAAGGGGCAT GACCCCTGAG   1680
TTATGAAGGG GAGAAGGGAC AGATGAGCTT CCGGAGACTG CTCTCCTCAC CACACAGCAC   1740
TAGTCCATCC TCAGCACCTG AGCCTCCCTC ACTTGGACAC TCAGGGACC ACACAGAGAA    1800
GTGGATGGAC ACTTCGCCAT CCAGGCAGAA CTAAGCCAGG CATAACCACA GCCAAGCAGA   1860
TTAACCCCAG GCAGACCGAT AAAAAGACCT CCAGATAGGC AGACAGACAG ATGGACCACC   1920
AACCTGGACA GACAGCCAAA GCTTCAGAGA TACAGTCCAC AGGTGGACAA AGGATCCCCC   1980
AGCCAGAGAG AGAGAGACCA GCCAACAGCT TGATAGACCA GTGCAGCCAG AGAGACCACC   2040
AAACACAGCC CCCAAAAGAC AGACATCTCT GCTAGCTGGA CAGCCAGGTG GACCCCCTAA   2100
GTTAGTCAGA TTACTAGACA GATATAAACA GATCCCCTGC TGAACAGATA TACAGAGTTC   2160
TCAGACCCCA CTCCCTCAGG TGGGCTGGCT GGCTGACAGA CCTTCTGGCC AGACAGACTC   2220
CTAACCAACC AGATGGACTG CCAGACAGGC AGACATCAGT CCACATGGAA TCCTGACATC   2280
CCAGCCAGCC GGCCAGACTC TCATCTTGAT GTCTTGATGG ATGGACCCCA GCTAGTCAGA   2340
CATGATCCTC CAGATTGACA GACAAGTCCC CCAAATGAGT ACACATCTCC AGCTATTCAG   2400
ACAGATGGAG CCCCAGCAAA TCAGGACCTA TCTAGGCAGA CCCCAGCCAG ACCCCCGCCA   2460
GACAGACTCC CAACCAGACT GACCCCTTGC TGTTCACACA GCCTGCCGAG TAGCTGGGAC   2520
TACAGGTCTA ATTTTTTTTT TTTTTAAGAA ATGAGTTTTT GCCATGTTGC CCAGACTGGT   2580
CTTGAACTCC CAACCTCAAG CAATCCTCCT GCCTCAGCCT CCCAAAGTGC TGAGATTACA   2640
GGTGTGAGCC ACCAGGCTCA GCCCCCTAAG ATTTGAAACA CTTTAAATGG CCCATGGTAG   2700
GGTTCCTGCT AGGATAAAAC ATTAAGTGGC TGTTAAAAGA AATAAAAGGA GGACACGTCT   2760
CTGTGCAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAA              2810
```

(2) INFORMATION FOR SEQ ID NO: 36:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 458 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

```
Met Ser Arg Ser Leu Asp Ser Ala Arg Ser Phe Leu Glu Arg Leu Glu
 1           5               10              15

Ala Arg Gly Gly Arg Glu Gly Ala Val Leu Ala Gly Glu Phe Ser Asp
        20              25              30

Ile Gln Ala Cys Ser Ala Ala Trp Lys Ala Asp Gly Val Cys Ser Thr
        35              40              45

Val Ala Gly Ser Arg Pro Glu Asn Val Arg Lys Asn Arg Tyr Lys Asp
    50              55              60

Val Leu Pro Tyr Asp Gln Thr Arg Val Ile Leu Ser Leu Leu Gln Glu
65              70              75              80

Glu Gly His Ser Asp Tyr Ile Asn Gly Asn Phe Ile Arg Gly Val Asp
            85              90              95

Gly Ser Leu Ala Tyr Ile Ala Thr Gln Gly Pro Leu Pro His Thr Leu
        100             105             110

Leu Asp Phe Trp Arg Leu Val Trp Glu Phe Gly Val Lys Val Ile Leu
        115             120             125

Met Ala Cys Arg Glu Ile Glu Asn Gly Arg Lys Arg Cys Glu Arg Tyr
    130             135             140

Trp Ala Gln Glu Gln Glu Pro Leu Gln Thr Gly Leu Phe Cys Ile Thr
145             150             155             160

Leu Ile Lys Glu Lys Trp Leu Asn Glu Asp Ile Met Leu Arg Thr Leu
            165             170             175

Lys Val Thr Phe Gln Lys Glu Ser Arg Ser Val Tyr Gln Leu Gln Tyr
        180             185             190

Met Ser Trp Pro Asp Arg Gly Val Pro Ser Ser Pro Asp His Met Leu
    195             200             205

Ala Met Val Glu Glu Ala Arg Arg Leu Gln Gly Ser Gly Pro Glu Pro
    210             215             220

Leu Cys Val His Cys Ser Ala Gly Cys Gly Arg Thr Gly Val Leu Cys
225             230             235             240

Thr Val Asp Tyr Val Arg Gln Leu Leu Leu Thr Gln Met Ile Pro Pro
            245             250             255

Asp Phe Ser Leu Phe Asp Val Val Leu Lys Met Arg Lys Gln Arg Pro
        260             265             270

Ala Ala Val Gln Thr Glu Glu Gln Tyr Arg Phe Leu Tyr His Thr Val
    275             280             285

Ala Gln Met Phe Cys Ser Thr Leu Gln Asn Ala Ser Pro His Tyr Gln
    290             295             300

Asn Ile Lys Glu Asn Cys Ala Pro Leu Tyr Asp Asp Ala Leu Phe Leu
305             310             315             320
```

```
Arg Thr Pro Gln Ala Leu Leu Ala Ile Pro Arg Pro Pro Gly Gly Val
            325                 330             335

Leu Arg Ser Ile Ser Val Pro Gly Ser Pro Gly His Ala Met Ala Asp
            340             345             350

Thr Tyr Ala Glu Glu Gln Lys Arg Gly Ala Pro Ala Gly Ala Gly Ser
            355             360             365

Gly Thr Gln Thr Gly Thr Gly Thr Gly Ala Arg Ser Ala Glu Glu Ala
            370             375             380

Pro Leu Tyr Ser Lys Val Thr Pro Arg Ala Gln Arg Pro Gly Ala His
385             390             395             400

Ala Glu Asp Ala Arg Gly Thr Leu Pro Gly Arg Val Pro Ala Asp Gln
            405             410             415

Ser Pro Ala Gly Ser Gly Ala Tyr Glu Asp Val Ala Gly Gly Ala Gln
            420             425             430

Thr Gly Gly Leu Gly Phe Asn Leu Arg Ile Gly Arg Pro Lys Gly Pro
            435             440             445

Arg Asp Pro Pro Ala Glu Trp Thr Arg Val
450             455
```

(2)   INFORMATION FOR SEQ ID NO: 37:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 503 amino acids
        (B)   TYPE: amino acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

```
Met Glu Pro Ala Gly Pro Ala Pro Gly Arg Leu Gly Pro Leu Leu Cys
1               5               10              15

Leu Leu Leu Ala Ala Ser Cys Ala Trp Ser Gly Val Ala Gly Glu Glu
            20              25              30

Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Ser Val Ala Ala Gly
            35              40              45

Glu Ser Ala Ile Leu His Cys Thr Val Thr Ser Leu Ile Pro Val Gly
            50              55              60

Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Ala Arg Glu Leu Ile Tyr
65              70              75              80

Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Glu Ser
            85              90              95

Thr Lys Arg Glu Asn Met Asp Phe Ser Ile Ser Ile Ser Asn Ile Thr
            100             105             110
```

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
          115   120   125

Pro Asp Thr Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val Arg
          130   135   140

Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala Arg Ala Thr
145   150   155   160

Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser Pro
                  165   170   175

Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser Asp
              180   185   190

Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser Tyr Ser Ile
          195   200   205

His Ser Thr Ala Lys Val Val Leu Thr Arg Glu Asp Val His Ser Gln
    210   215   220

Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu Arg
225   230   235   240

Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro Thr Leu Glu
              245   250   255

Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn Val Thr Cys
          260   265   270

Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr Trp Leu Glu
          275   280   285

Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val Thr Glu Asn
    290   295   300

Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Val Ser
305   310   315   320

Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu His Asp Gly
              325   330   335

Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser Ala His Pro
              340   345   350

Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly Ser Asn Glu
          355   360   365

Arg Asn Ile Tyr Ile Val Val Gly Val Val Cys Thr Leu Leu Val Ala
    370   375   380

Leu Leu Met Ala Ala Leu Tyr Leu Val Arg Ile Arg Gln Lys Lys Ala
385   390   395   400

Gln Gly Ser Thr Ser Ser Thr Arg Leu His Glu Pro Glu Lys Asn Ala
              405   410   415

Arg Glu Ile Thr Gln Asp Thr Asn Asp Ile Thr Tyr Ala Asp Leu Asn
              420   425   430

```
Leu Pro Lys Gly Lys Lys Pro Ala Pro Gln Ala Ala Glu Pro Asn Asn
        435             440             445

His Thr Glu Tyr Ala Ser Ile Gln Thr Ser Pro Gln Pro Ala Ser Glu
        450             455             460

Asp Thr Leu Thr Tyr Ala Asp Leu Asp Met Val His Leu Asn Arg Thr
465             470             475             480

Pro Lys Gln Pro Ala Pro Lys Pro Glu Pro Ser Phe Ser Glu Tyr Ala
            485             490             495

Ser Val Gln Val Pro Arg Lys
            500
```

(2)   INFORMATION FOR SEQ ID NO: 38:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 398 amino acids
        (B)   TYPE: amino acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

```
Met Pro Val Pro Ala Ser Trp Pro His Leu Pro Ser Pro Phe Leu Leu
 1           5               10              15

Met Thr Leu Leu Leu Gly Arg Leu Thr Gly Val Ala Gly Glu Asp Glu
        20              25              30

Leu Gln Val Ile Gln Pro Glu Lys Ser Val Ser Val Ala Ala Gly Glu
        35              40              45

Ser Ala Thr Leu Arg Cys Ala Met Thr Ser Leu Ile Pro Val Gly Pro
    50              55              60

Ile Met Trp Phe Arg Gly Ala Gly Ala Gly Arg Glu Leu Ile Tyr Asn
65              70              75              80

Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Glu Leu Thr
            85              90              95

Lys Arg Asn Asn Leu Asn Phe Ser Ile Ser Ile Ser Asn Ile Thr Pro
        100             105             110

Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser Pro
        115             120             125

Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val Arg
    130             135             140

Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Val Arg Ala Thr
145             150             155             160

Pro Glu His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser Pro
            165             170             175
```

Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser Asp
        180   185   190

Phe Gln Thr Asn Val Asp Pro Ala Gly Asp Ser Val Ser Tyr Ser Ile
        195   200   205

His Ser Thr Ala Arg Val Val Leu Thr Arg Gly Asp Val His Ser Gln
        210   215   220

Val Ile Cys Glu Met Ala His Ile Thr Leu Gln Gly Asp Pro Leu Arg
225   230   235   240

Gly Thr Ala Asn Leu Ser Glu Ala Ile Arg Val Pro Pro Thr Leu Glu
             245   250   255

Val Thr Gln Gln Pro Met Arg Ala Glu Asn Gln Ala Asn Val Thr Cys
        260   265   270

Gln Val Ser Asn Phe Tyr Pro Arg Gly Leu Gln Leu Thr Trp Leu Glu
        275   280   285

Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Leu Thr Glu Asn
        290   295   300

Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Thr Cys
305   310   315   320

Ala His Arg Asp Asp Val Val Leu Thr Cys Gln Val Glu His Asp Gly
             325   330   335

Gln Gln Ala Val Ser Lys Ser Tyr Ala Leu Glu Ile Ser Ala His Gln
        340   345   350

Lys Glu His Gly Ser Asp Ile Thr His Glu Pro Ala Leu Ala Pro Thr
        355   360   365

Ala Pro Leu Leu Val Ala Leu Leu Leu Gly Pro Lys Leu Leu Leu Val
        370   375   380

Val Gly Val Ser Ala Ile Tyr Ile Cys Trp Lys Gln Lys Ala
385   390   395